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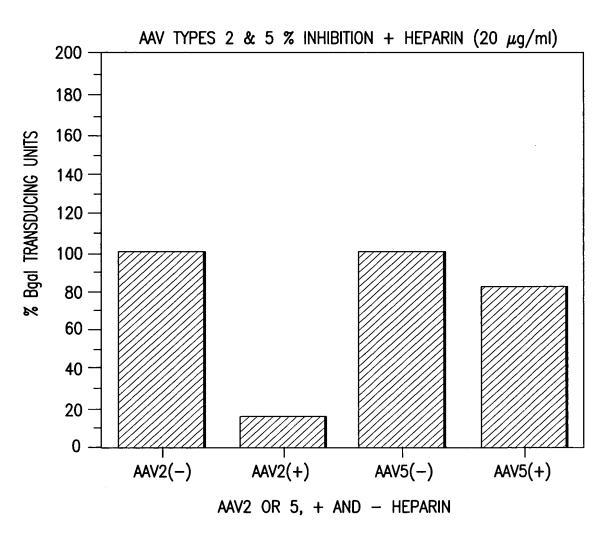
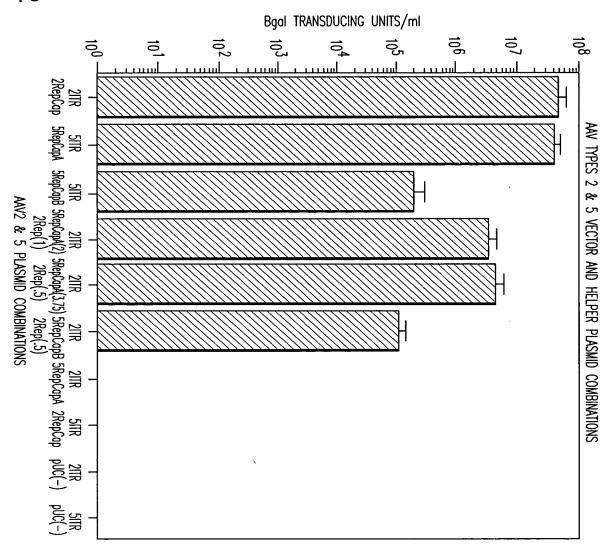


FIG.1



FIG.2





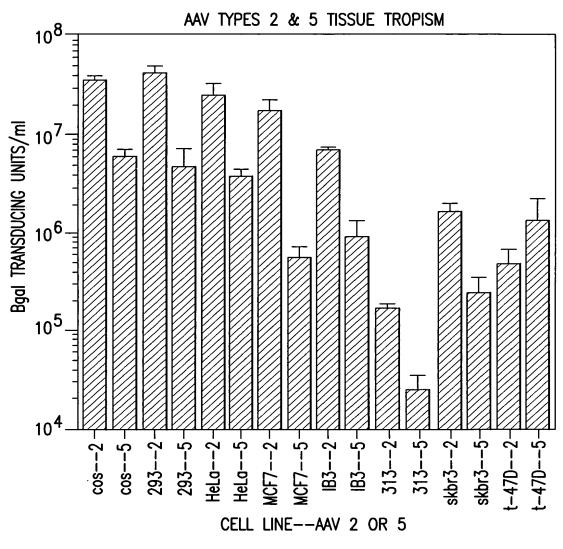


FIG.3

ALIGNMENT OF TWO NUCLEOTIDE SEQUENCES. THE TWO SEQUENCES TO BE ALIGNED ARE: AAV2CG. TOTAL NUMBER OF BASES: 4679. AAV5CG.TOTAL NUMBER OF BASES: 4652. OPEN GAP COST: 10 UNIT GAP COST: 12 THE CHARACTER TO SHOW THAT TWO ALIGNED RESIDUES ARE IDENTICIAL IS ":" AAV2CG - TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGA------GCCCGGGCGA -48 : : :::::: AAV2CG - C---CAAAGGTC-GCCCGACGCCCGGGCTTTGCCCGG-GCGGCCTCA----- -90 AAV5CG - CAGCTCAAAGAGCTGCCAGACGACGCCCTCTGGCCGTCGCCCCCAAACGAGC -110 AAV2CG - --GTGAGCGAGCGAGCGCG-CAGAGAGG-GAGTGGCCAACTCCATCACTAGGGGT -141 AAV2CG - TCCTGGAGGG-GTGGAGTCGTGACG-TGAATTACGTCATAGGGTTAGGGAGGTCC -194 AAV5CG - TTTTGTAAGCAGTGATGTCATAATGATGTAATGCTTATTGTCACGCGATAGTTAA -220 AAV2CG - TGTATTAGAGGTCACGTGA-GTGTTTTGCGACATTTTGCGACACC-----ATGT -242 AAV5CG - TG-ATTAACAGTCATGTGATGTGTTTTTATCCAATAGGAAGAAAGCGCGCGTATGA -274 AAV2CG - GGTCACGCT-----GGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCAT -288 : :: :::

FIG.4A

AAV5CG - GTTCTCGCGAGACTTCCGGGGTATAAAAGACCGAGTGAACGAGCCCGC-CGCCAT -328

AAV2CG	-	TGTGATTAAGGTCCCCAGCGACCTTGACGGGCATCTGCCCGGCATTTCTGACAGC	-395
AAV5CG	-	CATTGTTCGCGTCCCATTTGACGTGGAGGAACATCTGCCTGGAATTTCTGACAGC	-438
AAV2CG	-	TTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTTGCCGCCAGATTCTGACATGG	-450
AAV5CG	-	TTTGTGGACTGGGTAACTGGTCAAATTTGGGAGCTGCCTCCAGAGTCAGATTTAA	-493
AAV2CG	-	ATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGA	-505
AAV5CG	-	ATTTGACTCTGGTTGAACAGCCTCAGTTGACGGTGGCTGATAGAATTCGCCGCGT	-548
AAV2CG	-	CTTTCTGACGGAATGGCGCCGTGTGAGTAAGGCCCCGGAGGCCCTTTTCTTTGTG	-560
AAV5CG	-	GTTCCTGTACGAGTGGAACAAATTTTCCAAGCAGGAGTCCAAATTCTTTGTG	-600
AAV2CG	-	CAATTTGAGAAGGGAGAGAGCTACTTCCACATGCACGTGCTCGTGGAAACCACCG	-615
AAV5CG	-	CAGTTTGAAAAGGGATCTGAATATTTTCATCTGCACACGCTTGTGGAGACCTCCG	-655
AAV2CG	-	GGGTGAAATCCATGGTTTTGGGACGTTTCCTGAGTCAGATTCGCGAAAAACTGAT	
AAV5CG	-	GCATCTCTTCCATGGTCCTCGGCCGCTACGTGAGTCAGATTCGCGCCCAGCTGGT	
AAV2CG	-	TCAGAGAATTTACCGCGGGATCGAGCCGACTTTGCCAAACTGGTTCGCGGTCACA	-725
AAV5CG	-	GAAAGTGGTCTTCCAGGGAATTGAACCCCAGATCAACGACTGGGTCGCCATCACC	-765
AAV2CG	-	AAGACCAGAAATGGCGCCGGAGGCGGGAACAAGGTGGTGGATGAGTGCTACATCC	-780
AAV5CG	-	AAGGTAAAGAAGGGCGGAGCCAATAAGGTGGTGGATTCTGGGTATATTC	-814
AAV2CG	-	CCAATTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATAT	-835
AAV5CG	-	CCGCCTACCTGCCGAAGGTCCAACCGGAGCTTCAGTGGGCGTGGACAAACCT	-869
AAV2CG	-	GGAACAGTATTTAAGCGCCTGTTTGAATCTCACGGAGCGTAAACGGTTGGTGGCG	-890
AAV5CG	-	GGACGAGTATAAATTGGCCGCCCTGAATCTGGAGGAGCGCAAACGGCTCGTCGCG	-924

AAV2CG	-	CAGCATCTGACGCACGTGTCGCAGACGCAGGAGCAGAACAAAGAGAATCAGAATC	-945
AAV5CG	_	CAGTTTCTGGCAGAATCCTCGCAG-CGCTCGCAGGAGGCGGCTTCGCAGCGTG	-976
AAV2CG	-	CCAATTCTGATGCGCCGGTGATCAGATCAAAAACTTCAGCCAGGTACATGGAGCT	-1000
AAV5CG	-	AGTTCTCGGCTGACCCGGTCATCAAAAGCAAGACTTCCCAGAAATACATGGCGCT	-1031
AAV2CG	-	GGTCGGGTGGCTCGTGGACAAGGGGATTACCTCGGAGAAGCAGTGGATCCAGGAG	-1055
AAV5CG	-	CGTCAACTGGCTCGTGGAGCACGGCATCACTTCCGAGAAGCAGTGGATCCAGGAA	-1086
AAV2CG	-	GACCAGGCCTCATACATCTCCTTCAATGCGGCCTCCAACTCGCGGTCCCAAATCA	-1110
AAV5CG	-	AATCAGGAGAGCTACCTCTCCATCAACTCCACCGGCAACTCTCGGAGCCAGATCA	-1141
AAV2CG	-	AGGCTGCCTTGGACAATGCGGGAAAGATTATGAGCCTGACTAAAACCGCCCCCGA	-1165
AAV5CG	-	AGGCCGCGCTCGACAACGCGACCAAAATTATGAGTCTGACAAAAAGCGCGGTGGA	
AAV2CG	-	CTACCTGGTGGGCCAGCAGCCCGTG-GAGGACATTTCCAGCAATCGGATTTATAA	-1219
AAV5CG	-	CTACCTCGTGGGG-AGCTCCGTTCCCGAGGACATTTCAAAAAACAGAATCTGGCA	-1250
AAV2CG	_	AATTTTGGAACTAAACGGGTACGATCCCCAATATGCGGCTTCCGTCTTTCTGGGA	-1274
AAV5CG	_	AATTTTTGAGATGAATGGCTACGACCCGGCCTACGCGGGATCCATCC	-1305
AAV2CG	_	TGGGCCACGAAAAAGTTCGGCAAGAGGAACACCATCTGGCTGTTTGGGCCTGCAA	-1329
AAV5CG	-	TGGTGTCAGCGCTCCTTCAACAAGAGGAACACCGTCTGGCTCTACGGACCCGCCA	
AAV2CG	-	CTACCGGGAAGACCAACATCGCGGAGGCCATAGCCCACACTGTGCCCTTCTACGG	-1384
AAV5CG	-	CGACCGGCAAGACCAACATCGCGGAGGCCATCGCCCACACTGTGCCCTTTTACGG	-1415
AAV2CG	-	GTGCGTAAACTGGACCAATGAGAACTTTCCCTTCAACGACTGTGTCGACAAGATG	-1439
AAV5CG	-	CTGCGTGAACTGGACCAATGAAAACTTTCCCTTTAATGACTGTGTGGACAAAATG	-1470

AAV2CG	-	${\bf GTGATCTGGTGGGAGGGGGAAGATGACCGCCAAGGTCGTGGAGTCGGCCAAAG}\\$	-1494
AAV5CG	-	CTCATTTGGTGGGAGGGAAAGATGACCAACAAGGTGGTTGAATCCGCCAAGG	-1525
AAV2CG	-	CCATTCTCGGAGGAAGCAAGGTGCGCCGTGGACCAGAAATGCAAGTCCTCGGCCCA	-1549
AAV5CG	_	CCATCCTGGGGGGCTCAAAGGTGCGGGTCGATCAGAAATGTAAATCCTCTGTTCA	-1580
AAV2CG	-	GATAGACCCGACTCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATT	-1604
AAV5CG	-	AATTGATTCTACCCCTGTCATTGTAACTTCCAATACAAACATGTGTGTG	-1635
AAV2CG	-	GACGGGAACTCAACGACCTTCGAACACCAGCAGCCGTTGCAAGACCGGATGTTCA	-1659
AAV5CG	-	GATGGGAATTCCACGACCTTTGAACACCAGCAGCCGCTGGAGGACCGCATGTTCA	-1690
AAV2CG	-	AATTTGAACTCACCCGCCGTCTGGATCATGACTTTGGGAAGGTCACCAAGCAGGA	-1714
AAV5CG	-	AATTTGAACTGACTAAGCGGCTCCCGCCAGATTTTGGCAAGATTACTAAGCAGGA	-1745
AAV2CG	-	AGTCAAAGACTTTTTCCGGTGGGCAAAGGATCACGTGGTTGAGGTGGAGCATGAA	-1769
AAV5CG	-	AGTCAAGGACTTTTTTGCTTGGGCAAAGGTCAATCAGGTGCCGGTGACTCACGAG	-1800
AAV2CG	-	TTCTACGTCAAAAAGGGTGGAGCCAAGAAAAGACCCGCCCCAGTGACGCAGA	-1822
AAV5CG	-	TTTAAAGTTCCCAGGGAATTGGCGGGAACTAAAGGGGCGGAGAAATCTC	-1849
AAV2CG	-	TATAAGTGAGCCCAAACGGGTGCGCGAGTCAGTTGCGCAGCCATCGACGTCAGAC	
AAV5CG	-	TAAAACGCCCACT-GGGTGA-CGTCACCAATACT-AGCTATAAAAGTCTGGA	
AAV2CG	_	GCGGAAGCTTCGATCAACTACGCAGACAGGTACCAAAACAAAT-GTTCTCGTCAC	-1931
AAV5CG	-	GAAGCGGGCCAGGCTCTCATTT-GTTCCCGAGACGCCTCGCAGTTCAGAC	-1947
AAV2CG	-	GTGGGCATGAATCT-GATGCTGTTTCCCTGCAGACAATGCGAGAGAATGAATCAG	-1985
AAV5CG	-	GTGACTGTTGATCCCGCTCCTCTGCGACCGCTCA-ATTGGAATTCAAGGTATG	-1999

AAV2CG	- AATTCAAATATCTGCTTCACTCACGGACAGAAAGACTGTTTAGAGTGCTTTCCCG - : : : : : : : : : : : : : : : : : :	-2040
AAV5CG	- ATTGCAAATGTGACT-A-TCATGCTCAATTTGACAACATTTCTAACAAA -	-2046
AAV2CG	- TGTCA-GAATCTCAACCCGTTTCTGTCGTCAAAAAGGCGTATCAGAAACTGTG	-2092
AAV5CG	- TGTGATGAATGTGAATATTTGAATCGGGGCAAAAATGGATGTATCTGTCACAATG	-2101
AAV2CG	- CTACATTCA-TCATATCATGGGAAAGGTGCCAGACGCTTGCACTGCCTGCG	-2142
AAV5CG	- TAACTCACTGTCAAATTTGTCATGGGATTCCCCCCTGGGAAAAGGAAAACTTG	-2154
AAV2CG	- ATCTGGTCAATGTGGATTTGGATGACTGCATCTTTGAACAATAAATGATTTAAAT -	-2197
AAV5CG	- TCAGATTT-TGGGGATTTTGACGATGCCAATAAAGAACAGTAAATAAAGCGAGT	-2207
AAV2CG	- CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCT	-2252
AAV5CG	- AGTCATGTCTTTGTTGATCACCCTCCAGATTGGTTGGAAGAAGTTGGTGA	-2258
AAV2CG	- AGGAATAAGACAGTGGTGGAAGCTCAAACCTGGCCCACCACCACCAAAGCCCGCA -	-2307
AAV5CG	- AGGTCTTCGCGAGTTTTTGGGCCTTGAAGCGGGCCCACCGAAACCAAAACCCAAT -	-2313
AAV2CG	- GAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCTTCCTGGGTACAAGTACCTCG -	-2362
AAV5CG	- CAGCAGCATCAAGATCAAGCCCGTGGTCTTGTGCTGCCTGGTTATAACTATCTCG	-2368
AAV2CG	- GACCCTTCAACGGACTCGACAAGGGAGACCCGGTCAACGAGGCAGACGCCGGGC -	-2417
AAV5CG	- GACCCGGAAACGGTCTCGATCGAGGAGAGCCTGTCAACAGGGCAGACGAGGTCGC -	-2423
AAV2CG	- CCTCGAGCACGACAAGCCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTAC -	-2472
AAV5CG	- GCGAGAGCACGACATCTCGTACAACGAGCAGCTTGAGGCGGGAGACAACCCCTAC -	-2478
AAV2CG	- CTCAAGTACAACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGT -	-2527
AAV5CG	- CTCAAGTACAACCACGCGGACGCCGAGTTTCAGGAGAAGCTCGCCGACGACACAT -	-2533

AAV2CG	-	CTTTTGCGGGCAACCTCGGACGAGCAGTCTTCCAGGCGAAAAAGAGGGTTCTTGA	-2582
AAV5CG	-	CCTTCGGGGGAAACCTCGGAAAGGCAGTCTTTCAGGCCAAGAAAAGGGTTCTCGA	-2588
AAV2CG	-	ACCTCTGGGCCTGGTTGAGGAACCTGTTAAGACGGCTCCGGGAAAAAAAGAGGCCG	-2637
AAV5CG	-	ACCTTTTGGCCTGGTTGAAGAGGGTGCTAAGACGGCCCCTACCGGAAAGCGGATA	-2643
AAV2CG	-	GTAGAGCACTCTCCTGTGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCC	-2692
AAV5CG	-	GACGACCACTTTCCAAAA-AGAAAGAAGGCTCGGA-CCGAAGAGGACT-CC	-2691
		AGCAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGACGCAG-ACTCAG	
AAV5CG	-	: :::::: : : :::::::::::::::::::::::::	-2729
AAV2CG	_	TACCTGACCCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAAC	-2801
AAV5CG	-	CGGATCCC-AGCAGCTGCAAATCCCAGCCCAACCAGCCTCAAGTTTGGGAGC	-2780
AAV2CG	-	TAATACGATGCTACAGGCAGTGGCGCACCAATGGCAGACAATAACGAGGGCGCC	-2856
AAV5CG	-	TGATACAATGTCTGCGGGAGGTGGCGGCCCATTGGGCGACAATAACCAAGGTGCC	-2835
AAV2CG	-	GACGGAGTGGGTAATTCCTCGGGAAATTGGCATTGCGATTCCACATGGATGG	-2911
AAV5CG	-	GATGGAGTGGGCAATGCCTCGGGAGATTGGCATTGCGATTCCACGTGGATGGGGG	-2890
AAV2CG	-	ACAGAGTCATCACCACCAGCACCCGAACCTGGGCCCTGCCCACCTACAACAACCA	-2966
AAV5CG	-	ACAGAGTCGTCACCAAGTCCACCCGAACCTGGGTGCTGCCCAGCTACAACAACCA	-2945
AAV2CG	-	CCTCTACAAACAAATTTCCAGCCAATCAGGAGCCTCGAACGACAATCACTAC	-3018
AAV5CG	-	CCAGTACCGAGAGATCAAAAGCGGCTCCGTCGACGGAAGCAACGCCAACGCCTAC	-3000
AAV2CG	-	TTTGGCTACAGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACT	-3073
AAV5CG	_	TTTGGATACAGCACCCCTGGGGGTACTTTGACTTTAACCGCTTCCACAGCCACT	-3055

AAV2CG	-	TTTCACCACGTGACTGGCAAAGACTCATCAACAACAACTGGGGATTCCGACCCAA	-3128
AAV5CG	-	GGAGCCCCGAGACTGGCAAAGACTCATCAACAACTACTGGGGCTTCAGACCCCG	-3110
AAV2CG	-	GAGACTCAACTTCAAGCTCTTTAACATTCAAGTCAAAGAGGTCACGCAGAATGAC	-3183
AAV5CG	-	GTCCCTCAGAGTCAAAATCTTCAACATTCAAGTCAAAGAGGTCACGGTGCAGGAC	-3165
AAV2CG	-	GGTACGACGACTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGACT	-3238
AAV5CG	-	TCCACCACCACCATCGCCAACAACCTCACCTCCACCGTCCAAGTGTTTACGGACG	-3220
AAV2CG	-	CGGAGTACCAGCTCCCGTACGTCCTCGGCTCGGCGCATCAAGGATGCCTCCCGCC	-3293
AAV5CG	-	ACGACTACCAGCTGCCCTACGTCGGCAACGGGACCGAGGGATGCCTGCC	-3275
AAV2CG	-	GTTCCCAGCAGACGTCTTCATGGTGCCACAGTATGGATACCTCACCCTGAACAAC	
AAV5CG	_	CTTCCCTCCGCAGGTCTTTACGCTGCCGCAGTACGGTTACGCGACGCTGAACCGC	
AAV2CG	-	GGGAGT-CAGGCAGTAGGACGCTCTTCATTTTACTGCCTGGAGTACTTTC	-3397
AAV5CG	-	GACAACACAGAAAATCCCACCGAGAGGAGCAGCTTCTTCTGCCTAGAGTACTTTC	-3385
AAV2CG	-	CTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGCTACACTTTTGAGGA	-3452
AAV5CG	-	CCAGCAAGATGCTGAGAACGGGCAACAACTTTGAGTTTACCTACAACTTTGAGGA	-3440
AAV2CG	-	CGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAAT	-3507
AAV5CG	-	GGTGCCCTTCCACTCCAGCTTCGCTCCCAGTCAGAACCTGTTCAAGCTGGCCAAC	-3495
AAV2CG	-	CCTCTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAACACTC	-3553
AAV5CG	_	CCGCTGGTGGACCAGTACTTGTACCGCTTCGTGAGCACAAATAACACTGGCGGAG	-3550
AAV2CG	_	-CAAGTGGAACCACCACGCAGTCA-AGGCTTCAGTTTTCTCAGGCCGGAG	-3601
AAV5CG	-	: ::: ::: :: :: :: :: :: :: :: :: :: ::	-3605

AAV2CG	-	CGAGTGACATTCGGGACCAGTCTAGGAACTGGCTTCCTGGACCCTGTTACCGCCA	-3656
AAV5CG	-	CCCGGGGCCCATGGGCCGAACCCAGGG-CTGGAA-CCTGGGCTCCGGGGTCAACC	-3658
AAV2CG	-	GCAGCGAGTATCAAAGACATCTGCGGATAACAACAACAGTGAATACTCGTGGACT	-3711
AAV5CG	-	GC-GCCAGTGTCAGCGCCTTC-GCCACGACCAATAGGA-TGGAG-CTCGAGGGCG	-3709
AAV2CG	-	GGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGG	-3766
AAV5CG	-	CGAGTTACCAGGTGCCCCCGCAGCCGA-ACGGCATGACCAACAACCTCCAGG	-3760
AAV2CG	-	CCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTTTCCTCAGAGCGGGGTTCT	-3821
AAV5CG	-	GCAGCAACACCTATGCCCTGGAGAACACTATGATCTTCAACAGC-	-3804
AAV2CG	-	CATCTTTGGGAAGCAAGGCTCAGAGAAAACAAATGTGGACATTGAAAAGGTCATG	-3876
AAV5CG	-	CAGCCG-GCGAACCCGGGCACCACCGCCACGTACCTCGAGGGCAACATGCTCATC	-3858
AAV2CG	-	ATTACAGACGAAGAGGAAATCAGGACAACCAATCCCGTGGC-TACGGAGCAGTAT	-3930
AAV5CG	-	ACCAG-CGAGAGCGAGACGCAGCCGGTGAACCGCGTGGCGTACAACGTCGGCG	-3910
AAV2CG	-	GGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGCAGCTACCGCAGATG	-3985
AAV5CG	-	GGCAGA-TGGCCACCAACAACCAGAGCTCCACCACTGCCCCCGCGACCGGCACGT	-3964
AAy2CG	-	TCAACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCT	-4040
AAV5CG	-	ACAACCTCCAGGAAATCGTGCCCGGCAGCGTGTGGATGGA	-4019
AAV2CG	-	TCAGGGGCCCATCTGGGCAAAGATTCCACACACGGACGGA	-4095
AAV5CG	-	CCAAGGACCCATCTGGGCCAAGATCCCAGAGACGGGGGCGCACTTTCACCCCTCT	-4074
AAV2CG	-	CCCCTCATGGGTGGATTCGGACTTAAACACCCTCCTCCACAGATTCTCATCAAGA	-4150
AAV5CG	-	CCGGCCATGGGCGGATTCGGACTCAAACACCCACCGCCCATGATGCTCATCAAGA	-4129

AAV2CG	-	${\bf ACACCCCGGTACCTGCGAATCCTTCGACCACCTTCAGTG-CGGCAAAGTTTGCTT}$	-4204
AAV5CG	-	ACACGCCTGTGCCCGGAAATATC-ACCAGCTTCTCGGACGTGCCCGTCAGCAG	-4181
AAV2CG	-	${\bf CCTTCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAGTGGGAGCT}$	-4259
AAV5CG	-	C-TTCATCACCCAGTACAGCACCGGGCAGGTCACCGTGGAGATGGAGTGGGAGCT	-4235
AAV2CG	-	GCAGAAGGAAAACAGCAAACGCTGGAATCCCGAAATTCAGTACACTTCCAACTAC	-4314
AAV5CG	-	CAAGAAGGAAAACTCCAAGAGGTGGAACCCAGAGATCCAGTACACAAACAA	-4290
AAV2CG	-	AACAAGTCTGTTAATGTGGACTTTACTGTGGACACTAATGGCGTGTATTCAGAGC	-4369
AAV5CG	_	AACGACCCCAGTTTGTGGACTTTGCCCCGGACAGCACCGGGGAATACAGAAC	-4343
AAV2CG	-	CTCGCCCCATTGGCACCAGATACCTGACTCGTAATCTGTAATTGCTTGT-	-4418
AAV5CG	-	CACCAGACCTATCGGAACCCGATACCTTACCCGACCCCTTTAACCCATTCATGTC	-4398
AAV2CG	-	TAATCAATAAACCGTTTAATTCGTTTCAGTTGAACTTTGG-TCTCTGCGT	-4467
AAV5CG	-	GCATACCCTCAATAAACCGTGTA-TTCGTGTCAGTAAAATACTGCCTCTTGTGGT	-4452
AAV2CG	-	ATTTCTTTCT-TATCTAGTTTCCATGGCTAGATAAGTAGCATGGCGGGTTA	-4521
AAV5CG	-	CATTCAATGAATAACAGCTTACAACATCTACAAAACCTCCTTGCTTG	-4506
AAV2CG	-	ATCATTAACTACAAGGAACCCCTAGTGATGGAGTTGGCCACTCCCTC-TCTGCGC	-4575
AAV5CG	_	GGCACTCTCCCCCCTGTCGCGTTCGC-TCGCTCGCTGGCTCGTTTGGGG	-4554
AAV2CG	-	GCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTT	-4628
AAV5CG	-	GGGTGGCAGCTCAAAGAGCTGCCAGACGACGCCCTCTGGCCGTCGCCCC	-4604
AAV2CG	-	TGCCCGGGCGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAA -467	' 9
AAV5CG	_	CCCAAACGAGC-CAGCGAGCGAGCGAACGCGACAGGGGGGGAGAGTGCCA46	552

Identity : 3013 (64.77%)

Number of gaps inserted in AAV2CG: 43 Number of gaps inserted in AAV5CG: 63

FIG.4J

The two sequences to be aligned are:
AAV2VPI.
DE VPI
OS AAV2
Total number of residues: 735.
AAV5VP1.
DE AAV5VP1
OS AAV5VP1
Total number of residues: 724. 2101-4272
Comparison matrix : Structure-genetic matrix.
Open gap cost: 8
Unit gap cost: 5
The character to show that two aligned residues are identical is ':' The character to show that two aligned residues are similar is '.' Amino acids said to be 'similar' are: A,S,T; D,E; N,Q; R,K; I,L,M,V; F,Y,W
AAV2VP1 - MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGP -55
:. ::::: : : ::: :: : : :::::::::::::::
AAV5VP1 - MSFVDHPPDWLEE-VGEGLREFLGLEAGPPKPKPNQQHQDQARGLVLPGYNYLGP -54
AAV2VP1 - FNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSF -110
AAV5VP1 - GNGLDRGEPVNRADEVAREHDISYNEQLEAGDNPYLKYNHADAEFQEKLADDTSF -109
AAV2VP1 - GGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEPDSSSGTGKAGQQ -165
:::::::::::::::::::::::::::::::::::::::
AAV5VPI - GGNLGKAVFQAKKRVLEPFGLVEEGAKTAPTGKRIDDHFPKRKKARTEEDSKP -162

ALIGNMENT OF TWO PROTEIN SEQUENCES.

AAV2VP1	-	${\bf VGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNHLYKQISSQSG-ASNDNHYFG}$	-274
AAV5VP1	-	VGNASGDWHCDSTWMGDRVVTKSTRTWVLPSYNNHQYREIKSGSVDGSNANAYFG	-265
AAV2VP1	-	YSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGT	-329
AAV5VP1	-	YSTPWGYFDFNRFHSHWSPRDWQRLINNYWGFRPRSLRVKIFNIQVKEVTVQDST	-320
AAV2VP1	-	TTIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNGS	-384
AAV5VP1	_	TTIANNLTSTVQVFTDDDYQLPYVVGNGTEGCLPAFPPQVFTLPQYGYATLNRDN	-375
AAV2VP1	-	QAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPL	-437
AAV5VP1	-	TENPTERSSFFCLEYFPSKMLRTGNNFEFTYNFEEVPFHSSFAPSQNLFKLANPL	-430
		IDQYLYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTS	
AAV5VP1	-	VDQYLYRFVSTNNTGGVQFNKNLAGRYANTYKNWFPGPMGRTQGWNLGS	-479
AAV2VP1	-	ADNNNSEYSWTGATKYHLNGRDSLVNPGPAMASHKDDEEKFFPQSGVLIFGKQGS	-547
AAV5VP1	-	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	-534
AAV2VP1	-	EKTNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQG	-599
AAV5VP1	-	NPGTTATYLEGNMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQE	-589
AAV2VP1	-	VLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVP	-654
AV5VP1	-	IVPGSVWMERDVYLQGPIWAKIPETGAHFHPSPAMGGFGLKHPPPMMLIKNTPVP	-644
AAV2VP1	-	ANPSTTFSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVN	-709
AAV5VP1	-	: ::: ::::::::::::::::::::::::::::::::	-698
AAV2VP1		VDFTVDTNGVYSEPRPIGTRYLTRNL -735	
AV5VP1		:::. :: ::::::::::::::::::::::::::::::	

Identity: 421 (58.15%) Similarity: 63 (8.70%)

Number of gaps inserted in AAV2VP1: 3 Number of gaps inserted in AAV5VP1: 5

FIG.5C

The two sequences to be aligned are: REP78. DE REP78 OS AAV Total number of residues: 621. AAV5REP. DE REP OS AAV5 Total number of residues: 610. Comparison matrix: Structure-genetic matrix. Open gap cost: 8 Unit gap cost: 5 The character to show that two aligned residues are identical is ':' The character to show that two aligned residues are similar is '.' Amino acids said to be similar are: A,S,T; D,E; N,Q; R,K; I,L,M,V; F,Y,W REP78 - MPGFYEIVIKVPSDLDGHLPGISDSFVNWVAEKEWELPPDSDMDLNLIEQAPLTV -55 AAV5REP - MATFYEVIVRVPFDVEEHLPGISDSFVDWVTGQIWELPPESDLNLTLVEQPQLTV -55 REP78 - AEKLORDFLTEWRRVSKAPEALFFVOFEKGESYFHMHVLVETTGVKSMVLGRFLS -110 AAV5REP - ADRIRRVFLEWNKFSKRO-ESKFFVQFEKGSEYFHLHTLVETSGISSMVLGRYVS -109 REP78 - QIREKLIQRIYRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPEL -165 .. :::: . : :::: : : ::::: :::: :::: AAV5REP - QIRAQLVKVVFQGIEPQINDWVAITKVKKG--GANKVVDSGYIPAYLLPKVQPEL -162 REP78 - QWAWTNMEQYLSACLNLTERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKT -220 : : ::::::: AAV5REP - QWAWTNLDEYKLAALNLEERKRLVAQFLA-ESSQRSQEAASQREFSADPVIKSKT -216 REP78 - SARYMELVGWLVDKGITSEKQWIQEDQASYISFNAASNSRSQIKAALDNAGKIMS -275 AAV5REP - SQKYMALVNWLVEHGITSEKQWIQENQESYLSFNSTGNSRSQIKAALDNATKIMS -271

ALIGNMENT OF TWO PROTEIN SEQUENCES.

FIG.6A

REP78 - LTKTAPDYLVGQQPVEDISSNRIYKILELNGYDPQYAASVFLGWATKKFGKRNTI	-330
AAV5REP - LTKSAVDYLVGSSVPEDISKNRIWQIFEMNGYDPAYAGSILYGWCQRSFNKRNTV	-326
REP78 - WLFGPATTGKTNIAEAIAHTVPFYGCVNWTNENFPFNDCVDKMVIWWEEGKMTAK	-385
AAV5REP - WLYGPATTGKTNIAEAIAHTVPFYGCVNWTNENFPFNDCVDKMLIWWEEGKMTNK	-381
REP78 - VVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFEHQQP	-440
AAV5REP - VVESAKAILGGSKVRVDQKCKSSVQIDSTPVIVTSNTNMCVVVDGNSTTFEHQQP	-436
REP78 - LQDRMFKFELTRRLDHDFGKVTKQEVKDFFRWAKDHVVEVEHEFYVKKGGAKKRP	-495
AAV5REP - LEDRMFKFELTKRLPPDFGKITKQEVKDFFAWAKVNQVPVTHEFKVPRELAGTK-	-490
REP78 - APSDADISEPKRVRESVAQPSTSDAEASINYADRYQNKCSRHVGMNLMLFPVRQC	-550
AAV5REP - GAEKSLKRPLGDVTNTXYKSLEKRARLSFVPETPRSSDVTVDPAPLRPLNWNSRY	-545
REP78 - ERMNQNSNICFTHGQKDCLECFPVSESQPVSVVKKAYQKLCYIHHIMGKVPDACT	-605
AAV5REP - DC-KCDYHAQFDNISNKCDECEYLNRGKNGCICHNVTH-CQICHGIPPWEKENLS	-598
REP78 - ACDLVNVDLDDCIFEQ -621	
: :: :: AAV5REP - DFGDFDDANKEQ -610	
Identity: 355 (58.2%) Similarity: 56 (9.2%)	
Number of gaps inserted in REP78: 0 Number of gaps inserted in AAV5REP : 7	

FIG.6B

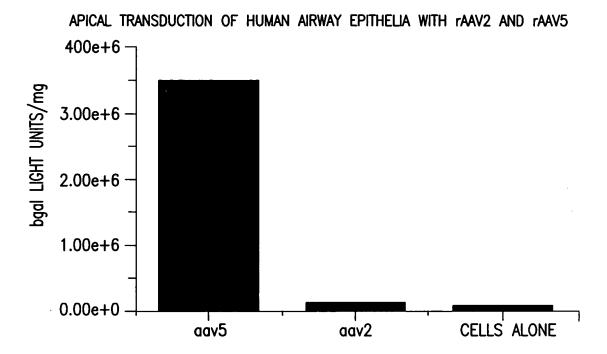
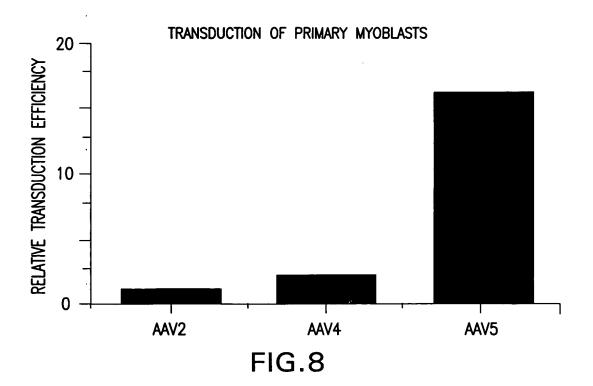


FIG.7



rAAV5 Primary Rat Brain Explant

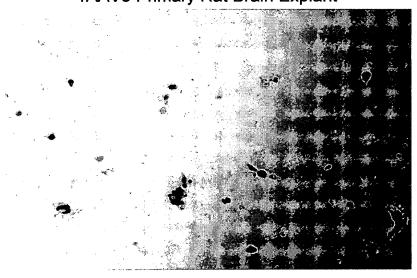


FIG.9

HUVEC

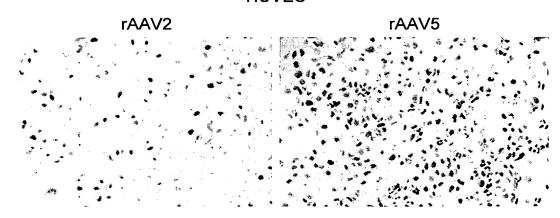


FIG.10

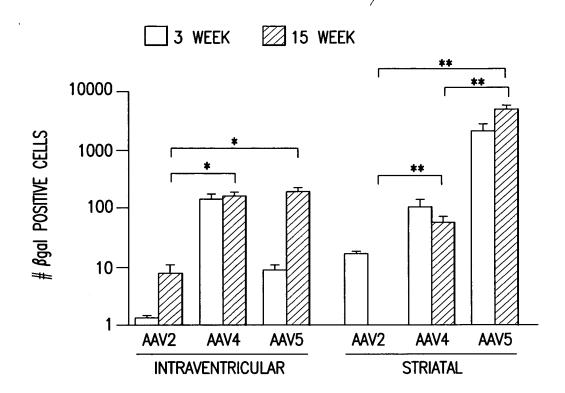
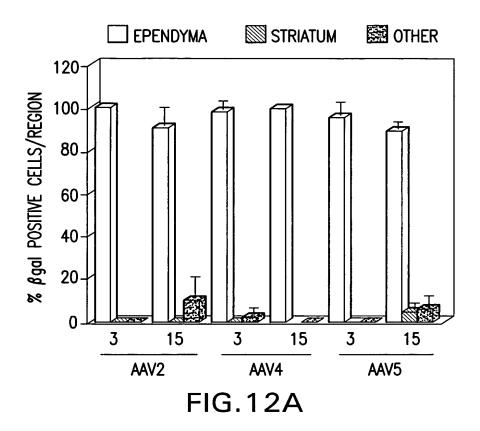
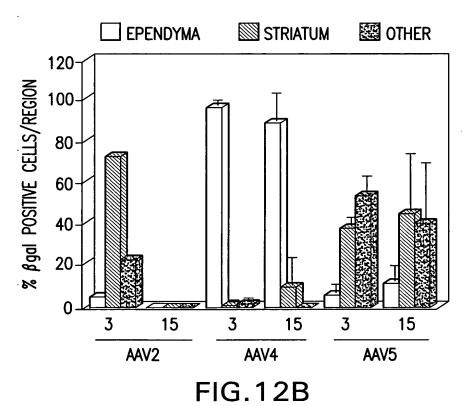
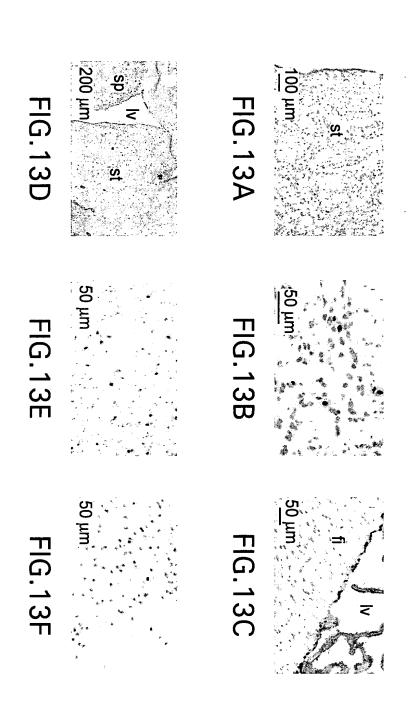


FIG.11







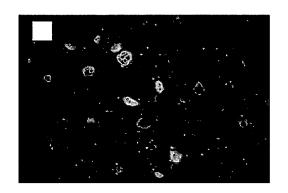


FIG.14A

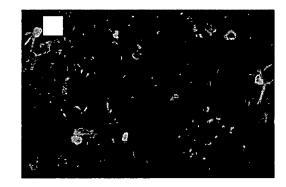


FIG.14B

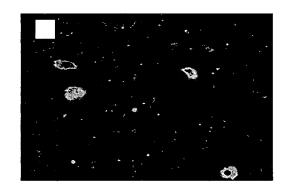


FIG.14C

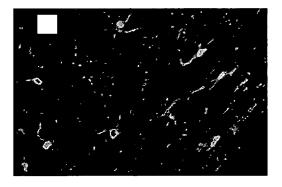
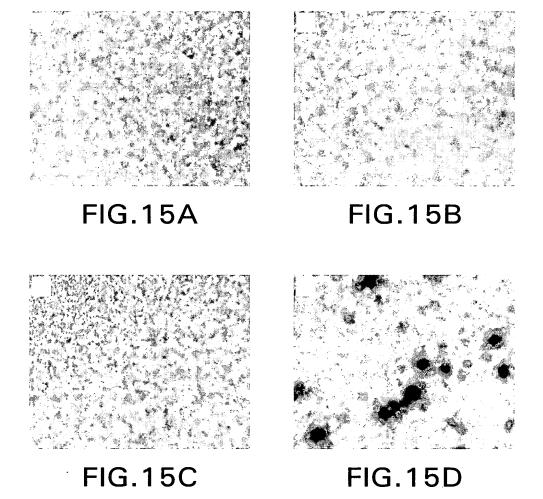


FIG.14D



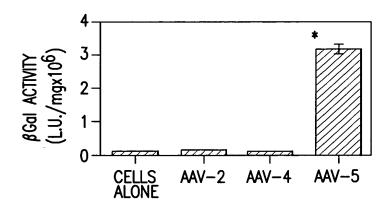
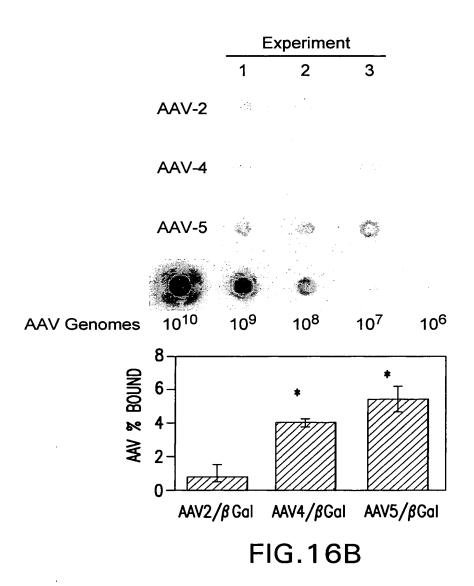


FIG.16A



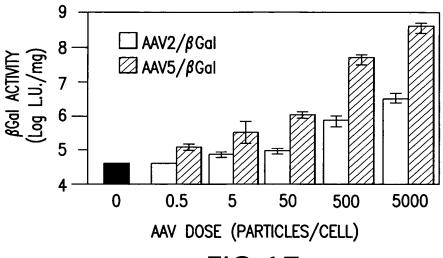


FIG.17

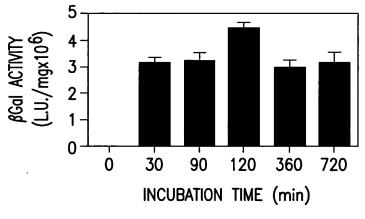
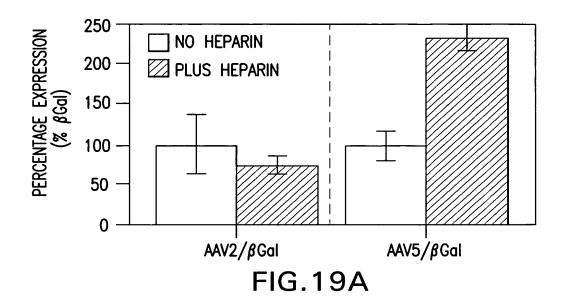
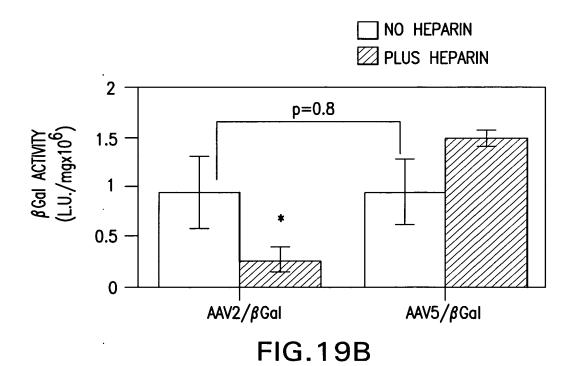


FIG.18





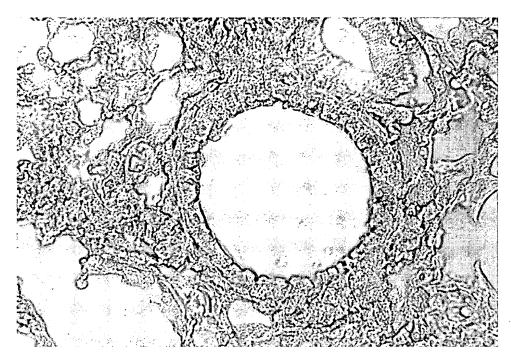


FIG.20A

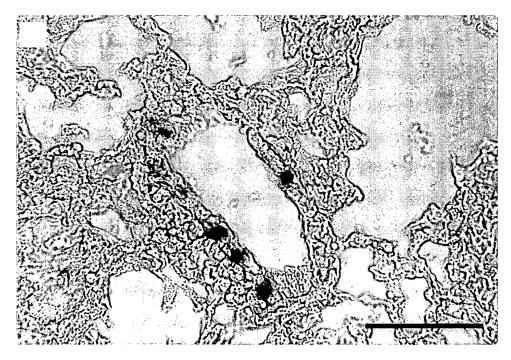
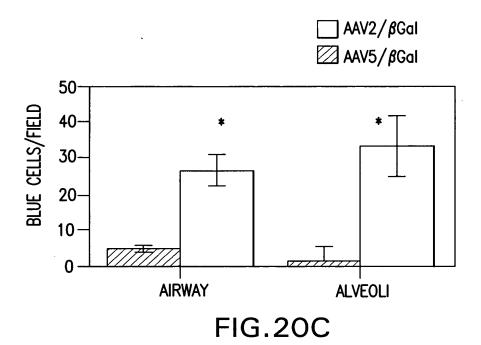


FIG.20B



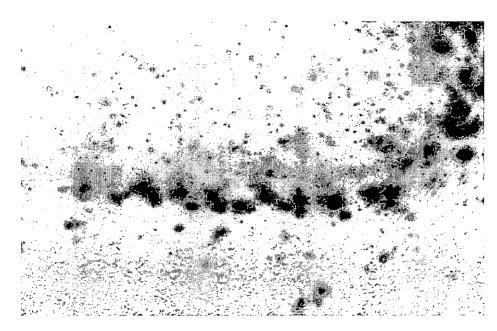


FIG.21

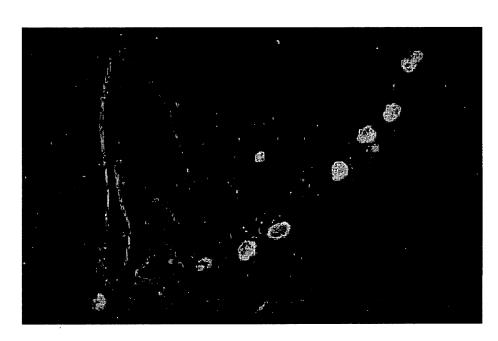


FIG.22

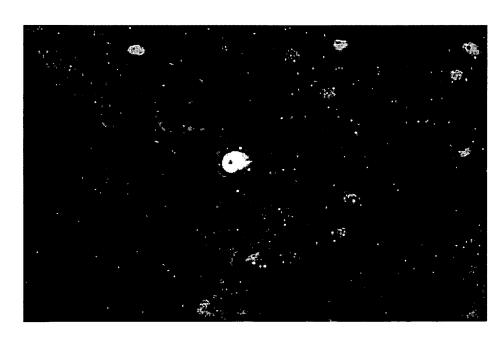


FIG.23

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